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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/578,063

DATE: 06/06/2000
TIME: 16:34:46

Input Set : A:\101476ul.app
Output Set: N:\CRF3\06062000\I578063.raw

ENTERED

3 <110> APPLICANT: McCarthy, Sean A
4 Barnes, Thomas M
5 Fraser, Christopher C
6 Sharp, John D
8 <120> TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC,
9 PREVENTIVE, THERAPEUTIC, AND OTHER USES
11 <130> FILE REFERENCE: 210147.0023/6U1
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/578,063
14 <141> CURRENT FILING DATE: 2000-05-24
16 <150> PRIOR APPLICATION NUMBER: US 09/333,159
17 <151> PRIOR FILING DATE: 1999-06-14
19 <160> NUMBER OF SEQ ID NOS: 79
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1656
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
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31 cccggacccg agtgtttcac agccaatggt gcggattata ggggaacaca gaactggaca 180
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33 actctgaaat accccaacgg ggaggggggc ctgggtgagc acaactattg cagaaatcca 300
34 gatggagacg tgagccccctg gtgctatgtg gcagagcagc aggatgggtg ctactggaag 360
35 tactgtgaga tacctgcttg ccagatgcct ggaacacctg gctgctacaa ggatcatgga 420
36 aaccacctc ctctaactgg caccagtaaa acgtccaaca aactcaccat acaaacttgc 480
37 atcagttttt gtcggagtca gaggttcaag tttgctggga tggagtcagg ctatgcttgc 540
38 ttctgtggaa acaatcctga ttactggaag tacggggagg cagccagtac cgaatgcaac 600
39 agcgtctgct tcggggatca ccccaaccc tgtggtggcg atggcaggat catctcttt 660
40 gatactctcg tgggcgcctg cgggtgggaac tactcagcca tgtcttctgt ggtctattcc 720
41 cctgacttcc ccgacaceta tgccacgggg agggctctgt actggaccat ccgggttccg 780
42 ggggcctccc acatccaact cagcttcccc ctatttgaca tcagggactc ggccgacatg 840
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44 ccacctctgt ccttcaacgt ctctctggac ttcgtcatct tgtatttctt ctctgacgc 960
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47 gtcagcgtcg ccggtcctc caaagtctc tatgtcatca ccaccagccc cagccacca 1140
48 cctcagactg tcccaggtag caattcctgg gcgccaccca tgggggctgg aagccacaga 1200
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55 tccctctgcc tcggcctctt cggggaaacc ctctctctac agactaggaa gaggcacctg 1620
56 ctgccagggc aggcagagcc tggattcctc ctgctt 1656
59 <210> SEQ ID NO: 2

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60 <211> LENGTH: 1425
61 <212> TYPE: DNA
62 <213> ORGANISM: Homo sapiens
64 <400> SEQUENCE: 2
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67 gattataggg gaacacagaa ctggacagca ctacaaggcg ggaagccatg tctgttttgg 180
68 aacgagactt tccagcatcc atacaacact ctgaaatacc ccaacgggga ggggggcctg 240
69 ggtgagcaca actattgcag aaatccagat ggagacgtga gccctggtg ctatgtggca 300
70 gagcacgagg atgggtgtcta ctggaagtac tgtgagatac ctgcttgcca gatgcctgga 360
71 aaccttggct gctacaagga tcatggaaac ccacctcctc taactggcac cagtaaaacg 420
72 tccaacaaac tcaccataca aacttgcata agtttttgtc ggagtcagag gttcaagtgt 480
73 gctgggatgg agtcaggcta tgcctgtctc tgtggaaaca atcctgatta ctggaagtac 540
74 ggggaggcag ccagtaccga atgcaacagc gtctgcttcg gggatcacac ccaaccctgt 600
75 ggtggcgatg gcaggatcat cctctttgat actctcgtgg gcgctgcgg tgggaactac 660
76 tcagccatgt cttctgtggt ctattcccct gacttccccg acacctatgc cacggggagg 720
77 gtctgtactt ggaccatccg ggttccgggg gcctcccaca tccacttcag cttccccccta 780
78 tttgacatca gggactcggc ggacatggtg gagcttctgg atggctacac ccaccgtgtc 840
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81 caagccgtca aggaagaact gccacaggag aggcgcgctg tcaaccagac ggtggccgag 1020
82 gtgatcacgg agcaggccaa cctcagtgtc agcgtgccc ggtcctccaa agtcctctat 1080
83 gtcacacaca ccagccccag ccaccacact cagactgtcc caggtagcaa ttccctggcg 1140
84 ccaccatgg gggctggaag ccacagagtt gaaggatgga cagtctatgg tctggcaact 1200
85 cctctcatcc tcacagtcaac agccattgta gcaaagatac ttctgcagct cacattcaaa 1260
86 tcccatcgtg ttctgtcttc aggggacctt agggattgtc atcaaccagg gacttcgggg 1320
87 gaaatctgga gcatttttta caagccttcc acttcaattt ccattcttaa gaagaaactc 1380
88 aagggtcaga gtcaacaaga tgaccgcaat cccctgtgta gtgac 1425
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92 <211> LENGTH: 475
93 <212> TYPE: PRT
94 <213> ORGANISM: Homo sapiens
96 <400> SEQUENCE: 3
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100 Thr Leu Ala Ala Arg Pro Ala Pro Ser Pro Gly Leu Gly Pro Gly Pro
101 20 25 30
103 Glu Cys Phe Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp
104 35 40 45
106 Thr Ala Leu Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe
107 50 55 60
109 Gln His Pro Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu
110 65 70 75 80
112 Gly Glu His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp
113 85 90 95
115 Cys Tyr Val Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu
116 100 105 110
118 Ile Pro Ala Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His
119 115 120 125

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121 Gly Asn Pro Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu
122      130      135      140
124 Thr Ile Gln Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe
125 145      150      155      160
127 Ala Gly Met Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp
128      165      170      175
130 Tyr Trp Lys Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys
131      180      185      190
133 Phe Gly Asp His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu
134      195      200      205
136 Phe Asp Thr Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser
137      210      215      220
139 Ser Val Val Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg
140 225      230      235      240
142 Val Cys Tyr Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe
143      245      250      255
145 Ser Phe Pro Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu
146      260      265      270
148 Leu Asp Gly Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser
149      275      280      285
151 Arg Pro Pro Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr
152      290      295      300
154 Phe Phe Ser Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr
155 305      310      315      320
157 Gln Ala Val Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln
158      325      330      335
160 Thr Val Ala Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala
161      340      345      350
163 Ala Arg Ser Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His
164      355      360      365
166 Pro Pro Gln Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly
167      370      375      380
169 Ala Gly Ser His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr
170 385      390      395      400
172 Leu Leu Ile Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His
173      405      410      415
175 Val Thr Phe Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp
176      420      425      430
178 Cys His Gln Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys
179      435      440      445
181 Pro Ser Thr Ser Ile Ser Ile Phe Lys Lys Lys Leu Lys Gly Gln Ser
182      450      455      460
184 Gln Gln Asp Asp Arg Asn Pro Leu Val Ser Asp
185 465      470      475
188 <210> SEQ ID NO: 4
189 <211> LENGTH: 19
190 <212> TYPE: PRT
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 4

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195 1 5 10 15
197 Thr Leu Ala
201 <210> SEQ ID NO: 5
202 <211> LENGTH: 456
203 <212> TYPE: PRT
204 <213> ORGANISM: Homo sapiens
206 <400> SEQUENCE: 5
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208 1 5 10 15
210 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu
211 20 25 30
213 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro
214 35 40 45
216 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu His
217 50 55 60
219 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val
220 65 70 75 80
222 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala
223 85 90 95
225 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro
226 100 105 110
228 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln
229 115 120 125
231 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met
232 130 135 140
234 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys
235 145 150 155 160
237 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp
238 165 170 175
240 His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp Thr
241 180 185 190
243 Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser Ser Val Val
244 195 200 205
246 Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys Tyr
247 210 215 220
249 Trp Thr Ile Arg Val Pro Gly Ala Ser His Ile His Phe Ser Phe Pro
250 225 230 235 240
252 Leu Phe Asp Ile Arg Asp Ser Ala Asp Met Val Glu Leu Leu Asp Gly
253 245 250 255
255 Tyr Thr His Arg Val Leu Ala Arg Phe His Gly Arg Ser Arg Pro Pro
256 260 265 270
258 Leu Ser Phe Asn Val Ser Leu Asp Phe Val Ile Leu Tyr Phe Phe Ser
259 275 280 285
261 Asp Arg Ile Asn Gln Ala Gln Gly Phe Ala Val Leu Tyr Gln Ala Val
262 290 295 300
264 Lys Glu Glu Leu Pro Gln Glu Arg Pro Ala Val Asn Gln Thr Val Ala
265 305 310 315 320
267 Glu Val Ile Thr Glu Gln Ala Asn Leu Ser Val Ser Ala Ala Arg Ser

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268          325          330          335
270 Ser Lys Val Leu Tyr Val Ile Thr Thr Ser Pro Ser His Pro Pro Gln
271          340          345          350
273 Thr Val Pro Gly Ser Asn Ser Trp Ala Pro Pro Met Gly Ala Gly Ser
274          355          360          365
276 His Arg Val Glu Gly Trp Thr Val Tyr Gly Leu Ala Thr Leu Leu Ile
277          370          375          380
279 Leu Thr Val Thr Ala Ile Val Ala Lys Ile Leu Leu His Val Thr Phe
280 385          390          395          400
282 Lys Ser His Arg Val Pro Ala Ser Gly Asp Leu Arg Asp Cys His Gln
283          405          410          415
285 Pro Gly Thr Ser Gly Glu Ile Trp Ser Ile Phe Tyr Lys Pro Ser Thr
286          420          425          430
288 Ser Ile Ser Ile Phe Lys Lys Lys Leu Lys Gly Gln Ser Gln Gln Asp
289          435          440          445
291 Asp Arg Asn Pro Leu Val Ser Asp
292          450          455
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296 <211> LENGTH: 373
297 <212> TYPE: PRT
298 <213> ORGANISM: Homo sapiens
300 <400> SEQUENCE: 6
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304 Thr Ala Asn Gly Ala Asp Tyr Arg Gly Thr Gln Asn Trp Thr Ala Leu
305          20          25          30
307 Gln Gly Gly Lys Pro Cys Leu Phe Trp Asn Glu Thr Phe Gln His Pro
308          35          40          45
310 Tyr Asn Thr Leu Lys Tyr Pro Asn Gly Glu Gly Gly Leu Gly Glu His
311          50          55          60
313 Asn Tyr Cys Arg Asn Pro Asp Gly Asp Val Ser Pro Trp Cys Tyr Val
314 65          70          75          80
316 Ala Glu His Glu Asp Gly Val Tyr Trp Lys Tyr Cys Glu Ile Pro Ala
317          85          90          95
319 Cys Gln Met Pro Gly Asn Leu Gly Cys Tyr Lys Asp His Gly Asn Pro
320          100          105          110
322 Pro Pro Leu Thr Gly Thr Ser Lys Thr Ser Asn Lys Leu Thr Ile Gln
323          115          120          125
325 Thr Cys Ile Ser Phe Cys Arg Ser Gln Arg Phe Lys Phe Ala Gly Met
326          130          135          140
328 Glu Ser Gly Tyr Ala Cys Phe Cys Gly Asn Asn Pro Asp Tyr Trp Lys
329 145          150          155          160
331 Tyr Gly Glu Ala Ala Ser Thr Glu Cys Asn Ser Val Cys Phe Gly Asp
332          165          170          175
334 His Thr Gln Pro Cys Gly Gly Asp Gly Arg Ile Ile Leu Phe Asp Thr
335          180          185          190
337 Leu Val Gly Ala Cys Gly Gly Asn Tyr Ser Ala Met Ser Ser Val Val
338          195          200          205
340 Tyr Ser Pro Asp Phe Pro Asp Thr Tyr Ala Thr Gly Arg Val Cys Tyr

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VERIFICATION SUMMARY

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Input Set : A:\101476u1.app

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number